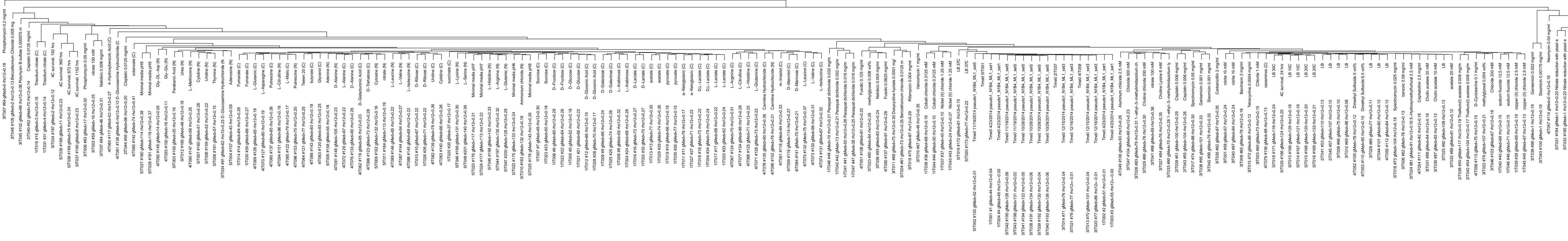


Height

0.0
0.2
0.4
0.6
0.8



as.dist(1 - cor(log2(1 + fit\$G[fit\$NS]locusId %in% fit\$genesUsed, hclust("c", fit\$D[fit\$NS]complete)))